FIGURE 1A

```
   1 GAGGGTGGAAGCCGGGGTCTCGCGGGCCGCGGGCCGCATGACTCCTCTCTGCCTCAATTG   60
  61 CTCTGTCCTCCCTGGAGACCTGTACCCAGGGGGTGCAAGGAACCCCATGGCTTGCAATGG  120
 121 CAGTGCGGCCAGGGGGCACTTTGACCCTGAGGACTTGAACCTGACTGACGAGGCACTGAG  180
 181 ACTCAAGTACCTGGGGCCCCAGCAGACAGAGCTGTTCATGCCCATCTGTGCCACATACCT  240
 241 GCTGATCTTCGTGGTGGGCGCTGTGGGCAATGGGCTGACCTGTCTGGTCATCCTGCGCCA  300
 301 CAAGGCCATGCGCACGCCTACCAACTACTACCTCTTCAGCCTGGCCGTGTCGGACCTGCT  360
 361 GGTGCTGCTGGTGGGCCTGCCCCTGGAGCTCTATGAGATGTGGCACAACTACCCCTTCCT  420
 421 GCTGGGCGTTGGTGGCTGCTATTTCCGCACGCTACTGTTTGAGATGGTCTGCCTGGCCTC  480
 481 AGTGCTCAACGTCACTGCCCTGAGCGTGGAACGCTATGTGGCCGTGGTGCACCCACTCCA  540
 541 GGCCAGGTCCATGGTGACGCGGGCCCATGTGCGCCGAGTGCTTGGGGCCGTCTGGGGTCT  600
 601 TGCCATGCTCTGCTCCCTGCCCAACACCAGCCTGCACGGCATCCGGCAGCTGCACGTGCC  660
 661 CTGCCGGGGCCCAGTGCCAGACTCAGCTGTTTGCATGCTGGTCCGCCCACGGGCCCTCTA  720
```

FIGURE 1B

```
721 CAACATGGTAGTGCAGACCACCGCGCTGCTCTTCTTCTGCCTGCCCATGGCCATCATGAG   780

781 CGTGCTCTACCTGCTCATTGGGCTGCGACTGCGGCGGGAGAGGCTGCTGCTCATGCAGGA   840

841 GGCCAAGGGCAGGGGCTCTGCAGCAGCCAGGTCCAGATACACCTGCAGGCTCCAGCAGCA   900

901 CGATCGGGGCCGGAGACAAGTGACCAAGATGCTGTTTGTCCTGGTCGTGGTGTTTGGCAT   960

961 CTGCTGGGCCCCGTTCCACGCCGACCGCGTCATGTGGAGCGTCGTGTCACAGTGGACAGA  1020

1021 TGGCCTGCACCTGGCCTTCCAGCACGTGCACGTCATCTCCGGCATCTTCTTCTACCTGGG  1080

1081 CTCGGCGGCCAACCCCGTGCTCTATAGCCTCATGTCCAGCCGCTTCCGAGAGACCTTCCA  1140

1141 GGAGGCCCTGTGCCTCGGGGCCTGCTGCCATCGCCTCAGACCCCGCCACAGCTCCCACAG  1200

1201 CCTCAGCAGGATGACCACAGGCAGCACCCTGTGTGATGTGGGCTCCCTGGGCAGCTGGGT  1260

1261 CCACCCCCTGGCTGGGAACGATGGCCCAGAGGCGCAGCAAGAGACCGATCCATCCTGA    1318
```

FIGURE 2A

1	M	T	P	L	C	L	N	C	S	V	L	P	G	D	L	Y	P	G	G	A	20
21	R	N	P	M	A	C	N	G	S	A	A	R	G	H	F	D	P	E	D	L	40
41	N	L	T	D	E	A	L	R	L	K	Y	L	G	P	Q	Q	T	E	L	F	60
61	M	P	I	C	A	T	Y	L	L	I	F	V	V	G	A	V	G	N	G	L	80
81	T	C	L	V	I	L	R	H	K	A	M	R	T	P	T	N	Y	Y	L	F	100
101	S	L	A	V	S	D	L	L	V	L	L	V	G	L	P	L	E	L	Y	E	120
121	M	W	H	N	Y	P	F	L	L	G	V	G	G	C	Y	F	R	T	L	L	140
141	F	E	M	V	C	L	A	S	V	L	N	V	T	A	L	S	V	E	R	Y	160
161	V	A	V	V	H	P	L	Q	A	R	S	M	V	T	R	A	H	V	R	R	180
181	V	L	G	A	V	W	G	L	A	M	L	C	S	L	P	N	T	S	L	H	200
201	G	I	R	Q	L	H	V	P	C	R	G	P	V	P	D	S	A	V	C	M	220
221	L	V	R	P	R	A	L	Y	N	M	V	V	Q	T	T	A	L	L	F	F	240

FIGURE 2B

241	C L P M A I M S V L Y L L I G L R L R R	260
261	E R L L L M Q E A K G R G S A A A R S R	280
281	Y T C R L Q Q H D R G R R Q V T K M L F	300
301	V L V V V F G I C W A P F H A D R V M W	320
321	S V V S Q W T D G L H L A F Q H V H V I	340
341	S G I F F Y L G S A A N P V L Y S L M S	360
361	S R F R E T F Q E A L C L G A C C H R L	380
381	R P R H S S H S L S R M T T G S T L C D	400
401	V G S L G S W V H P L A G N D G P E A Q	420
421	Q E T D P S	426

FIGURE 3A

```
   1  AGGGGAGGCTCAGGCCTTGGATTTTAATGTCAGGGATGGAAAAACTTCAGAATGCTTCCT   60
  61  GGATCTACCAGCAGAAACTAGAAGATCCATTCCAGAAACACCTGAACAGCACCGAGGAGT  120
 121  ATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCACTTCTTCCTCCCCGTGTCTGTGGTGT  180
 181  ATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGC  240
 241  AGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCTGGCGGTCTCTGACC  300
 301  TCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAACTACCCTT  360
 361  TCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTGTGCTTCG  420
 421  CCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGT  480
 481  TCCGCGCCAAACTGCAGAGCACCCGGCGCCGGGCCCTCAGGATCCTCGGCATCGTCTGGG  540
 541  GCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTCCACTACT  600
 601  TCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACCTGTACGGTCATCAAGCCCATGTGGA  660
 661  TCTACAATTTCATCATCCAGGTCACCTCCTTCCTATTCTACCTCCTCCCCATGACTGTCA  720
```

FIGURE 3B

```
721  TCAGTGTCCTCTACTACCTCATGGCACTCAGACTAAAGAAAGACAAATCTCTTGAGGCAG  780
781  ATGAAGGGAATGCAAATATTCAAAGACCCTGCAGAAAATCAGTCAACAAGATGCTGTTTG  840
841  TCTTGGTCTTAGTGTTTGCTATCTGTTGGGCCCCGTTCCACATTGACCGACTCTTCTTCA  900
901  GCTTTGTGGAGGAGTGGAGTGAATCCCTGGCTGCTGTGTTCAACCTCGTCCATGTGGTGT  960
961  CAGGTGTCTTCTTCTACCTGAGCTCAGCTGTCAACCCCATTATCTATAACCTACTGTCTC 1020
1021 GCCGCTTCCAGGCAGCATTCCAGAATGTGATCTCTTCTTTCCACAAACAGTGGCACTCCC 1080
1081 AGCATGACCCACAGTTGCCACCTGCCCAGCGGAACATCTTCCTGACAGAATGCCACTTTG 1140
1141 TGGAGCTGACCGAAGATATAGGTCCCCAATTCCCATGTCAGTCATCCATGCACAACTCTC 1200
1201 ACCTCCCAACAGCCCTCTCTAGTGAACAGATGTCAAGAACAAACTATCAAAGCTTCCACT 1260
1261 TTAACAAAACCTGAATTCTTTCAGAGCTGACTCTCCTC                        1298
```

FIGURE 4A

1	M	S	G	M	E	K	L	Q	N	A	S	W	I	Y	Q	Q	K	L	E	D	20
21	P	F	Q	K	H	L	N	S	T	E	E	Y	L	A	F	L	C	G	P	R	40
41	R	S	H	F	F	L	P	V	S	V	V	Y	V	P	I	F	V	V	G	V	60
61	I	G	N	V	L	V	C	L	V	I	L	Q	H	Q	A	M	K	T	P	T	80
81	N	Y	Y	L	F	S	L	A	V	S	D	L	L	V	L	L	L	G	M	P	100
101	L	E	V	Y	E	M	W	R	N	Y	P	F	L	F	G	P	V	G	C	Y	120
121	F	K	T	A	L	F	E	T	V	C	F	A	S	I	L	S	I	T	T	V	140
141	S	V	E	R	Y	V	A	I	L	H	P	F	R	A	K	L	Q	S	T	R	160
161	R	R	A	L	R	I	L	G	I	V	W	G	F	S	V	L	F	S	L	P	180
181	N	T	S	I	H	G	I	K	F	H	Y	F	P	N	G	S	L	V	P	G	200
201	S	A	T	C	T	V	I	K	P	M	W	I	Y	N	F	I	I	Q	V	T	220
221	S	F	L	F	Y	L	L	P	M	T	V	I	S	V	L	Y	Y	L	M	A	240

FIGURE 4B

241	L	R	L	K	K	D	K	S	L	E	A	D	E	G	N	A	N	I	Q	R	260
261	P	C	R	K	S	V	N	K	M	L	F	V	L	V	L	V	F	A	I	C	280
281	W	A	P	F	H	I	D	R	L	F	F	S	F	V	E	E	W	S	E	S	300
301	L	A	A	V	F	N	L	V	H	V	V	S	G	V	F	F	Y	L	S	S	320
321	A	V	N	P	I	I	Y	N	L	L	S	R	R	F	Q	A	A	F	Q	N	340
341	V	I	S	S	F	H	K	Q	W	H	S	Q	H	D	P	Q	L	P	P	A	360
361	Q	R	N	I	F	L	T	E	C	H	F	V	E	L	T	E	D	I	G	P	380
381	Q	F	P	C	Q	S	S	M	H	N	S	H	L	P	T	A	L	S	S	E	400
401	Q	M	S	R	T	N	Y	Q	S	F	H	F	N	K	T						415

FIGURE 5

```
            .         .         .         .         .
  1 MTPLCLNCSVLPGDLYPGGARNPMACNGSAARGHFDP..EDLNLTDEALR  48
                    |         .    .    ||  . || |:|.|
  1 ................MSGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLA  34
            .         .         .         .         .
 49 LKYLGPQQTELFMPICATYLLIFVVGAVGNGLTCLVILRHKAMRTPTNYY  98
     ||...  |:|:    |. ||||| :||  | |||||.|.||:||||||
 35 F.LCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYY  83
            .         .         .         .         .
 99 LFSLAVSDLLVLLVGLPLELYEMWHNYPFLLGVGGCYFRTLLFEMVCLAS 148
    ||||||||||||.|:|||.||||  |||||  |   ||||:| ||| || ||
 84 LFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFAS 133
            .         .         .         .         .
149 VLNVTALSVERYVAVVHPLQARSMVTRAHVRRVLGAVWGLAMLCSLPNTS 198
    :|.:|  .||||||||:.||  .|:    ||     |:|| |||  ..| ||||||
134 ILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS 183
            .         .         .         .         .
199 LHGIRQLHVPCRGPVPDSAVCMLVRPRALYNMVVQTTALLFFCLPMAIMS 248
    :|||:  :  |     || || |  .::|  :|| ::| |. ||: ||| :.|
184 IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVIS 233
            .         .         .         .         .
249 VLYLLIGLRLRRERLLLMQEAKGRGSAAARSRYTCRLQQHDRGRRQVTKM 298
    ||| |. |||::::  |     |         |  .  |          |: | ||
234 VLYYLMALRLKKDKSLEADEGN......ANIQRPC........RKSVNKM 269
            .         .         .         .         .
299 LFVLVVVFGICWAPFHADRVMWSVVSQWTDGLHLAFQHVHVISGIFFYLG 348
    |||||.|| ||||||| ||.  .| | :|.: |     |   |||:||:||||
270 LFVLVLVFAICWAPFHIDRLFFSFVEEWSESLAAVFNLVHVVSGVFFYLS 319
            .         .         .         .         .
349 SAANPVLYSLMSSRFRETFQEAL.CLGACCH.....RLRPRHSSHSLSRM 392
    || ||::|.|:| ||.  ||   :         |      .| |    .  |.
320 SAVNPIIYNLLSRRFQAAFQNVISSFHKQWHSQHDPQLPPAQRNIFLTEC 369
            .         .         .         .
393 TTGSTLCDVGSLGSWVHPLAGNDGPEAQQETDPS............ 426
          |:|           :  .  | |       |
370 HFVELTEDIGPQFPCQSSMHNSHLPTALSSEQMSRTNYQSFHFNKT 415
```

FIGURE 6

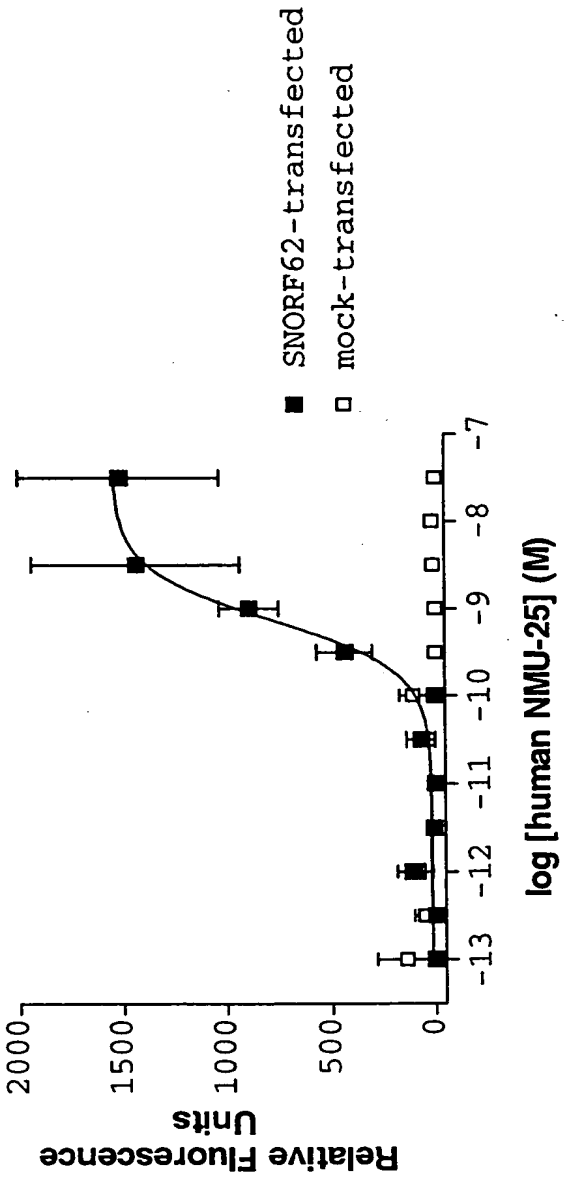
SNORF62-transfected
mock-transfected
Relative Fluorescence Units
2000
1500
1000
500
0
-13
-12
-11
-10
-9
-8
-7
log [human NMU-25] (M)

FIGURE 7

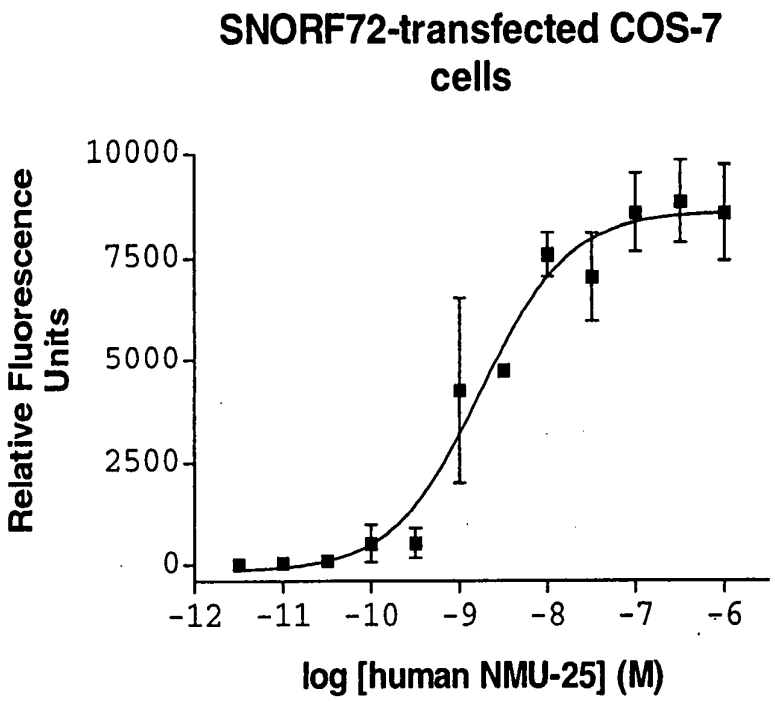
SNORF72-transfected COS-7 cells
Relative Fluorescence Units
10000
7500
5000
2500
0
-12
-11
-10
-9
-8
-7
-6
log [human NMU-25] (M)

FIGURE 8

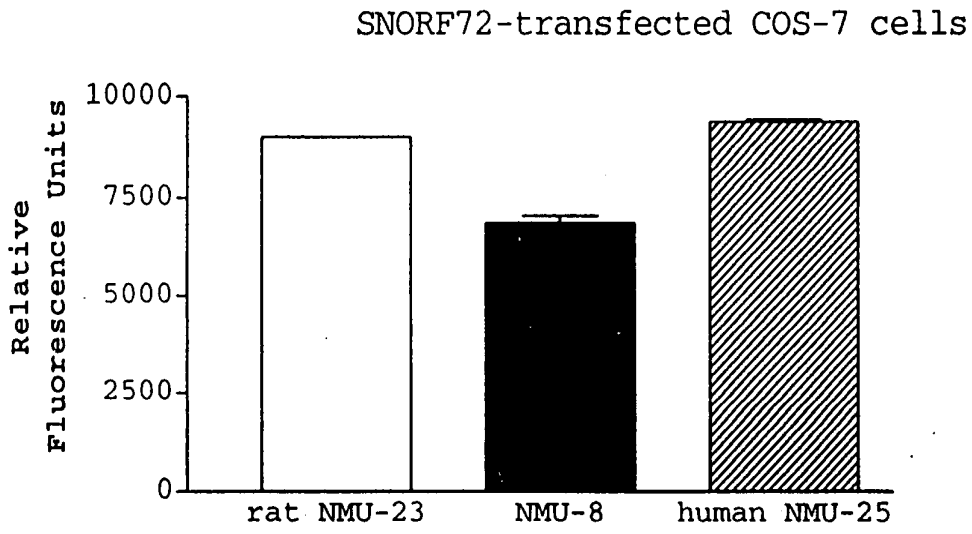

FIGURE 9A

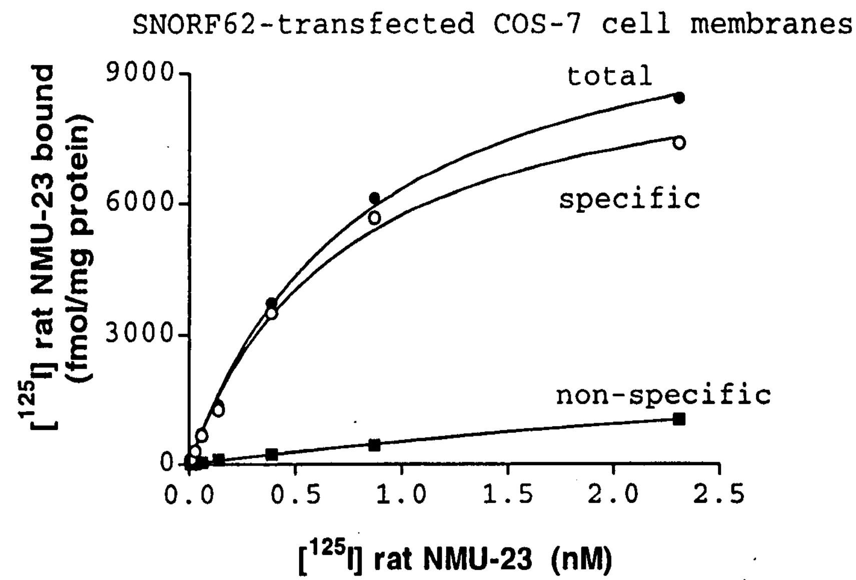

FIGURE 9B

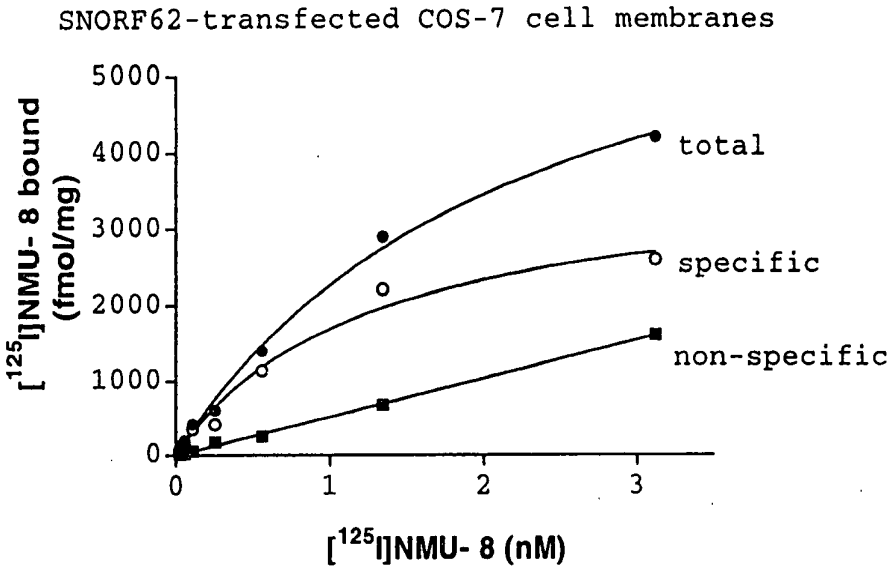

FIGURE 10

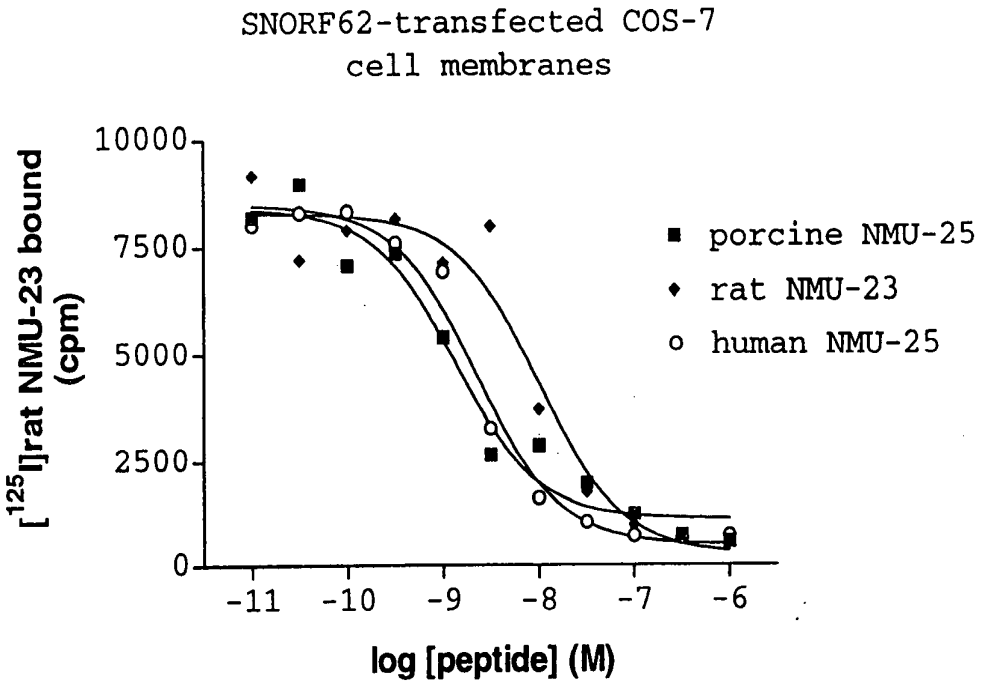
SNORF62-transfected COS-7
cell membranes
10000
7500
5000
2500
0
[125I]rat NMU-23 bound
(cpm)
-11
-10
-9
-8
-7
-6
log [peptide] (M)
porcine NMU-25
rat NMU-23
human NMU-25

FIGURE 11A

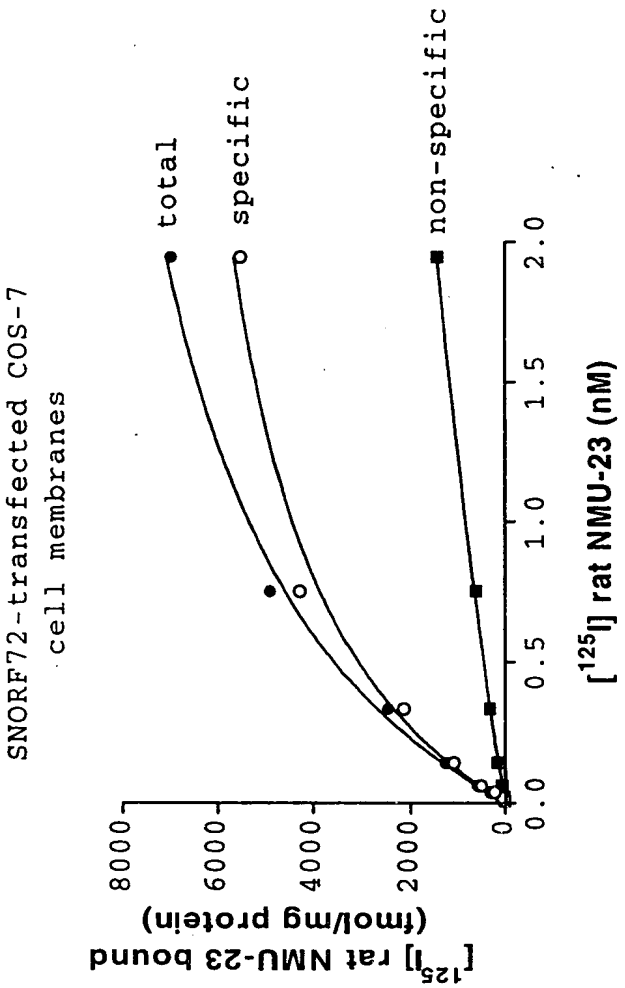

FIGURE 11B

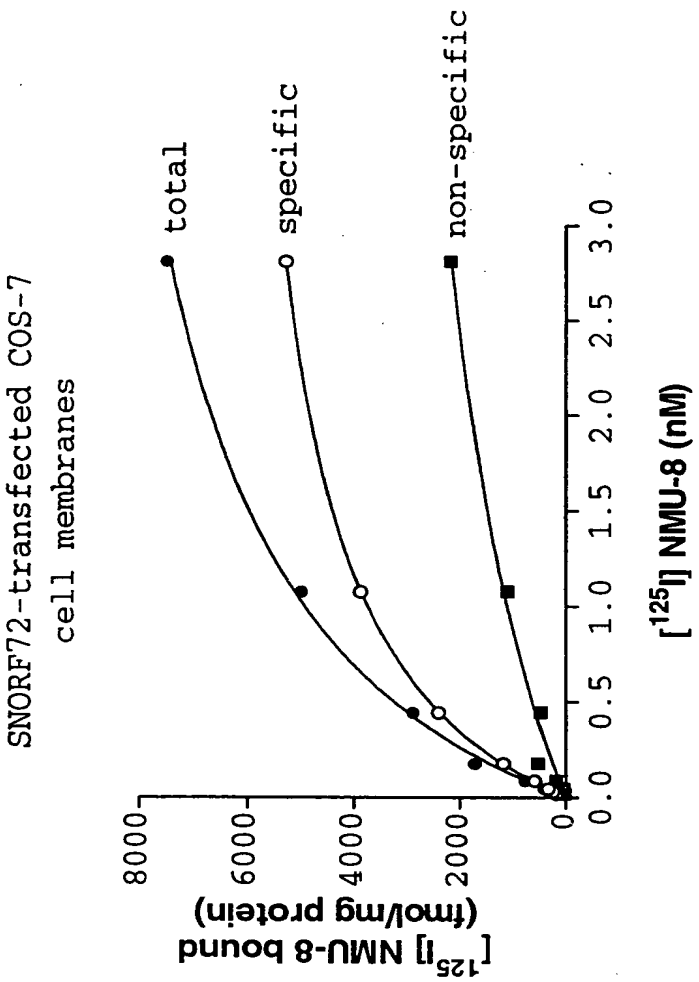

FIGURE 12

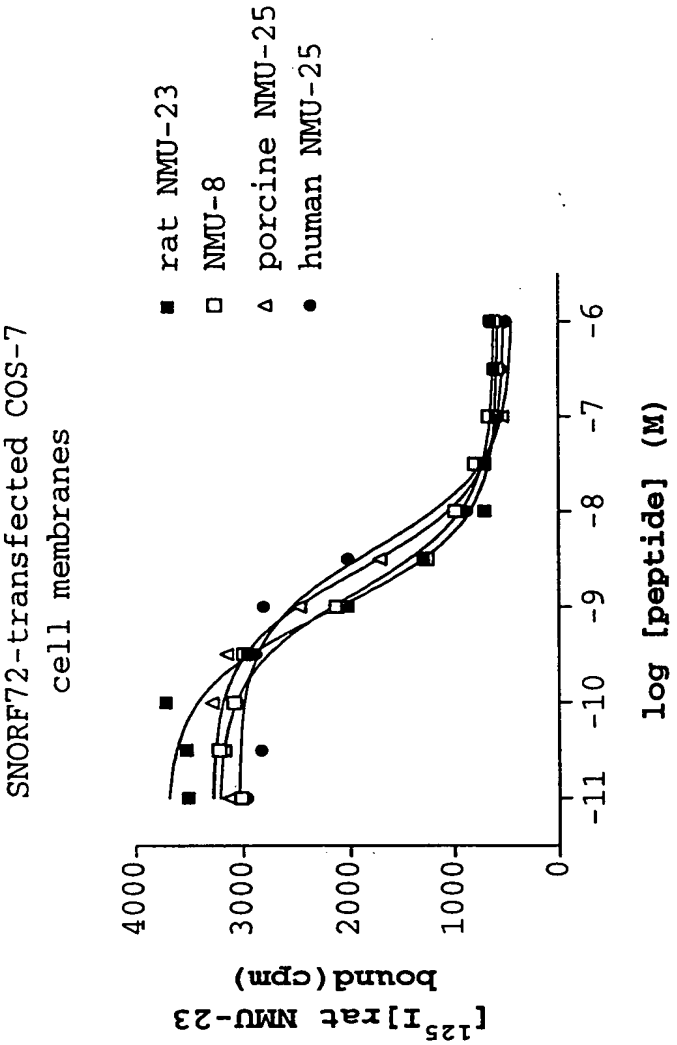

FIGURE 13

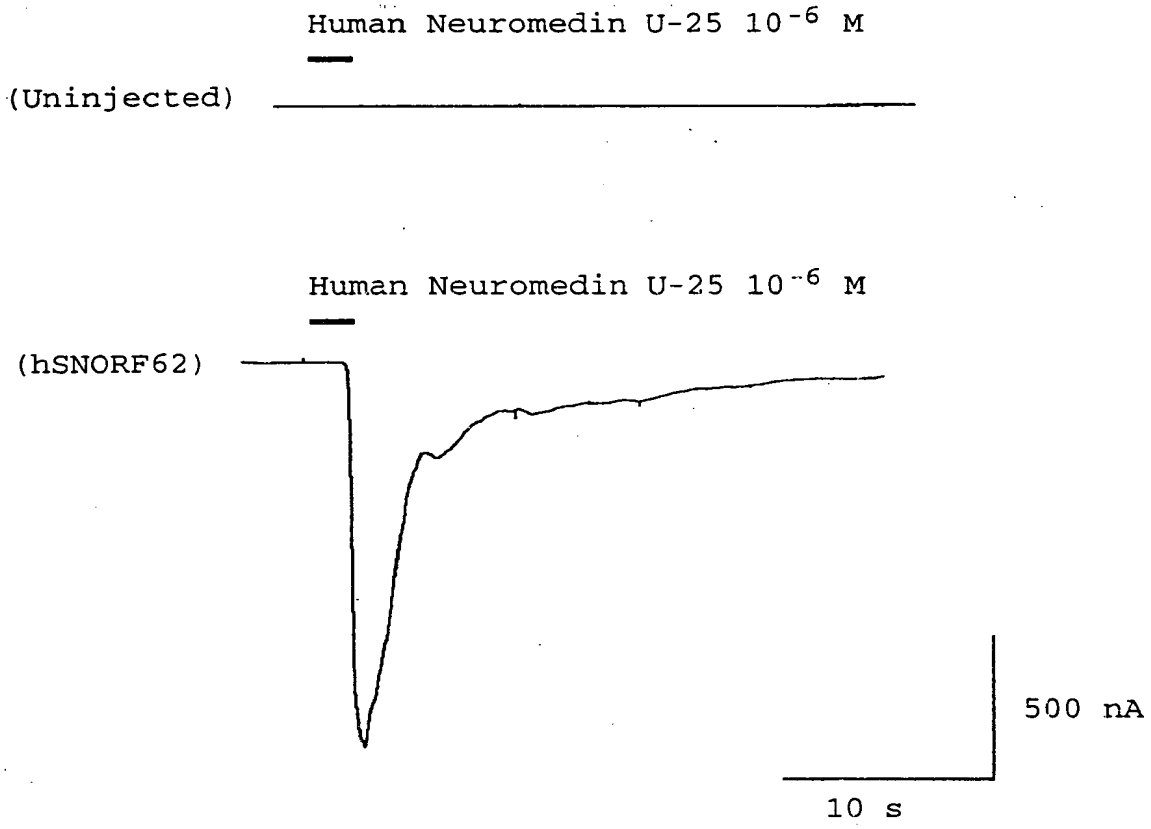

FIGURE 14A

```
  1  GTTGTGGATTTTAAGCTCAGTAATGGGAAAACTTGAAAATGCTTCCTGGATCCACGATCC   60
 61  TCTCATGAAGTACTTGAACAGCACAGAGGAGTACTTGGCCCACCTGTGTGGACCCAAGCG  120
121  CAGTGACCTATCCCTTCCGGTGTCTGTGGCCTATGCGCTGATCTTCCTGGTGGGGGTAAT  180
181  GGGCAATCTTCTGGTGTGCATGGTGATTGTCCGACATCAGACTTTGAAGACACCCACCAA  240
241  CTACTATCTCTTCAGCTTGGCAGTCTCAGATCTGCTGGTCCTGCTCTTGGGGATGCCTCT  300
301  GGAAATCTACGAGATGTGGCACAATTACCCTTTCCTGTTCGGGCCTGTGGGATGCTACTT  360
361  CAAGACAGCCCTCTTCGAGACTGTGTGCTTTGCCTCCATTCTCAGTGTCACCACGGTTAG  420
421  CGTAGAGCGCTATGTGGCCATTGTCCACCCTTTCCGAGCCAAGCTGGAGAGCACGCGGCG  480
481  ACGGGCCCTCAGGATCCTCAGCCTAGTCTGGAGCTTCTCTGTGGTCTTTTCTTTGCCCAA  540
541  TACCAGCATCCATGGCATCAAGTTCCAGCACTTTCCCAACGGGTCCTCCGTACCTGGCTC  600
601  AGCCACCTGCACAGTCACCAAACCCATGTGGGTGTATAACTTGATCATCCAAGCTACCAG  660
661  CTTCCTCTTCTACATCCTCCCAATGACCCTCATCAGCGTCCTCTACTACCTCATGGGGCT  720
```

FIGURE 14B

721	CAGGCTGAAGAGAGATGAATCCCTTGAGGCGAACAAAGTGGCTGTGAATATTCACAGACC	780
781	CTCTAGAAAGTCAGTCACCAAGATGCTGTTTGTCTTGGTCCTCGTGTTTGCCATCTGCTG	840
841	GACCCCCTTCCATGTGGACCGGCTCTTCTTCAGCTTTGTGGAAGAGTGGACAGAGTCCCT	900
901	GGCTGCTGTGTTCAACCTCATCCATGTGGTATCAGGTGTCTTCTTTTATCTGAGCTCCGC	960
961	GGTCAACCCCATTATCTATAACCTCCTGTCTCGGCGCTTCCGGGCGGCCTTTCGAAATGT	1020
1021	TGTCTCCCCTACCTGCAAATGGTGCCATCCCCGGCATCGGCCACAGGGACCTCCAGCCCA	1080
1081	GAAGATCATCTTCTTGACAGAATGTCACCTCGTGGAGCTGACAGAGGATGCAGGCCCCCA	1140
1141	GTTCCCTGGTCAGTCATCCATCCACAACACCAACCTTACCACGGCCCCCTGTGCAGGAGA	1200
1201	GGTACCATAAAAGGAGTGGTCAGAAGGCCTC	1231

FIGURE 15A

```
 1 M G K L E N A S W I H D P L M K Y L N S  20
21 T E E Y L A H L C G P K R S D L S L P V  40
41 S V A Y A L I F L V G V M G N L L V C M  60
61 V I V R H Q T L K T P T N Y Y L F S L A  80
81 V S D L L V L L L G M P L E I Y E M W H 100
101 N Y P F L F G P V G C Y F K T A L F E T 120
121 V C F A S I L S V T T V S V E R Y V A I 140
141 V H P F R A K L E S T R R R A L R I L S 160
161 L V W S F S V V F S L P N T S I H G I K 180
181 F Q H F P N G S S V P G S A T C T V T K 200
201 P M W V Y N L I I Q A T S F L F Y I L P 220
221 M T L I S V L Y Y L M G L R L K R D E S 240
```

FIGURE 15B

241	L	E	A	N	K	V	A	V	N	I	H	R	P	S	R	K	S	V	T K	260
261	M	L	F	V	L	V	L	V	F	A	I	C	W	T	P	F	H	V	D R	280
281	L	F	F	S	F	V	E	E	W	T	E	S	L	A	A	V	F	N	L I	300
301	H	V	V	S	G	V	F	F	Y	L	S	S	A	V	N	P	I	I	Y N	320
321	L	L	S	R	R	F	R	A	A	F	R	N	V	V	S	P	T	C	K W	340
341	C	H	P	R	H	R	P	Q	G	P	P	A	Q	K	I	I	F	L	T E	360
361	C	H	L	V	E	L	T	E	D	A	G	P	Q	F	P	G	Q	S	S I	380
381	H	N	T	N	L	T	T	A	P	C	A	G	E	V	P	*				395

FIGURE 16A

```
SNORF72_RAT    ~~~~~~~~~~ ~~~~~~~~~~M GKLENASWIH .....DPLMK YLNSTEEYLA
SNORF72_HUMAN  ~~~~~~~~~~ ~~~~~~MSGM EKLQNASWIY QQKLEDPFQK HLNSTEEYLA
SNORF62_HUMAN  MTPLCLNCSV LPGDLYPGGA RNPMACNGSA ARGHFDP..E DLNLTDEALR

SNORF72_RAT    H.LCGPKRSD LSLPVSVAYA LIFLVGVMGN LLVCMVIVRH QTLKTPTNYY
SNORF72_HUMAN  F.LCGPRRSH FFLPVSVVYV PIFVVGVIGN VLVCLVILQH QAMKTPTNYY
SNORF62_HUMAN  LKYLGPQQTE LFMPICATYL LIFVVGAVGN GLTCLVILRH KAMRTPTNYY

SNORF72_RAT    LFSLAVSDLL VLLLGMPLEI YEMWHNYPFL FGPVGCYFKT ALFETVCFAS
SNORF72_HUMAN  LFSLAVSDLL VLLLGMPLEV YEMWRNYPFL FGPVGCYFKT ALFETVCFAS
SNORF62_HUMAN  LFSLAVSDLL VLLVGLPLEL YEMWHNYPFL LGVGGCYFRT LLFEMVCLAS

SNORF72_RAT    ILSVTTVSVE RYVAIVHPFR AKLESTRRRA LRILSLVWSF SVVFSLPNTS
SNORF72_HUMAN  ILSITTVSVE RYVAILHPFR AKLQSTRRRA LRILGIVWGF SVLFSLPNTS
SNORF62_HUMAN  VLNVTALSVE RYVAVVHPLQ ARSMVTRAHV RRVLGAVWGL AMLCSLPNTS

SNORF72_RAT    IHGIKFQHFP NGSSVPGSAT CTVTKPMWVY NLIIQATSFL FYILPMTLIS
SNORF72_HUMAN  IHGIKFHYFP NGSLVPGSAT CTVIKPMWIY NFIIQVTSFL FYLLPMTVIS
SNORF62_HUMAN  LHGIRQLHVP CRGPVPDSAV CMLVRPRALY NMVVQTTALL FFCLPMAIMS
```

FIGURE 16B

```
SNORF72_RAT     VLYYLMGLRL KRDESL...E A...NKVAVN IHRPS..... ...RKSVTKM
SNORF72_HUMAN   VLYYLMALRL KKDKSL...E A...DEGNAN IQRPC..... ...RKSVNKM
SNORF62_HUMAN   VLYLLIGLRL RRERLLLMQE AKGRGSAAAR SRYTCRLQQH DRGRRQVTKM

SNORF72_RAT     LFVLVLVFAI CWTPFHVDRL FFSFVEEWTE SLAAVFNLIH VVSGVFFYLS
SNORF72_HUMAN   LFVLVLVFAI CWAPFHIDRL FFSFVEEWSE SLAAVFNLVH VVSGVFFYLS
SNORF62_HUMAN   LFVLVVVFGI CWAPFHADRV MWSVVSQWTD GLHLAFQHVH VISGIFFYLG

SNORF72_RAT     SAVNPIIYNL LSRRFRAAFR NV..VSPTCK WCHPRHRPQG PPAQKIIFLT
SNORF72_HUMAN   SAVNPIIYNL LSRRFQAAFQ NV..ISSFHK QWHSQHDPQL PPAQRNIFLT
SNORF62_HUMAN   SAANPVLYSL MSSRFRETFQ EALCLGACCH RLRPRHSSH. SLSRMTTGST

SNORF72_RAT     ECHLVELTED AGPQFPGQSS IHNTNLTTAP CAGEVP~~~~ ~~~~~~~~
SNORF72_HUMAN   ECHFVELTED IGPQFPCQSS MHNSHLPTAL SSEQMSRTNY QSFHFNKT
SNORF62_HUMAN   LCDVGSLGSW VHPLAGNDGP EAQQETDPS~ ~~~~~~~~~~ ~~~~~~~~
```

FIGURE 17A

```
   1  CACCATCTCGGTTTAAGATAAAGATATGGAGCTCTCCCCAAATGCTTCAACGGGCCTCTT   60
  61  GTCCTGCAATGACAGTGAGTTCAAGGAGCACTTTGACCTTGAGGACCTGAACCTTACTCA  120
 121  TGAGGACCTGAGGCTGAAGTACTTGGGGCCACAGCAGGTAAAACAATTTTTGCCCATCTG  180
 181  TGTCACGTACCTGTTGATCTTCGTAGTGGGCACTCTGGGCAACGGGTTGACCTGCACCGT  240
 241  CATCCTGCGCCAGAAGGCAATGCACACGCCCACCAACTTCTACCTCTTCAGTCTCGCGGT  300
 301  GTCCGATTTGCTGGTGCTCCTGGTGGGCTTGCCCCTGGAACTTTATGAGATGCAGCACAA  360
 361  TTACCCATTCCAGCTGGGTGCAGGTGGCTGTTACTTCCGGATACTGCTTTTGGAGACTGT  420
 421  CTGCCTGGCTTCAGTGCTCAATGTCACAGCCCTAAGTGTGGAGCGTTATGTGGCCGTGGT  480
 481  GCACCCACTCCAAGCCAAGTCTGTGATGACACGGACCCATGTGCGCCGCATGTTGGGAGC  540
 541  CATCTGGGTCTTCGCTATTCTCTTCTCTCTGCCCAACACCAGCTTACATGGCCTCAGTCC  600
 601  ACTCTATGTACCCTGCCGGGGGCCGGTGCCCGATTCAGTTACGTGTACGCTGGTGCGTCC  660
 661  CCAGTTCTTCTACAAGTTGGTAATACAGACGACCATACTGCTCTTCTTCTGTCTGCCCAT  720
```

FIGURE 17B

```
721  GGTCACCATCAGTGTGCTGTACCTGCTCATTGGGCTGAGGCTGCGGAGGGAGAGGATGTT  780
781  GCTCCAAGAGGAGGTCAAGGGCAGGATATCTGCAGCAGCCAGGCAGGCCTCCCACAGAAG  840
841  TATTCAGCTTCGAGATAGGGAACGCAGACAGGTGACCAAGATGCTAATTGCTCTGGTTAT  900
901  AGTATTTGGCACCTGCTGGGTTCCATTCCATGCTGACCGTCTCATGTGGAGTATGGTGTC  960
961  CCATTGGACTGACGGCCTGCGCCTGGCCTTCCAGTCTGTGCACCTTGCTTCTGGTGTCTT 1020
1021 CTTGTACCTCGGCTCAGCGGCTAACCCGGAGCTCTACAACCTCATGTCCACTCGCTTCCG 1080
1081 AGAGTCCTTCCGGGAAACCCTGGGCCTTGGGACACGGTGCTGTCATCGCCACCAACCGCG 1140
1141 TCACGACTCCCATAGCCACCTTAGGTTGACCACAGTCAGCACCCTGTGTGACAGGAACAG 1200
1201 CAGGGATGTACCCCTGGCTGAGAACAGGGATCCAGGGTGTGAGCAAGAGACAGACCCTCC 1260
1261 TGAATAAAATCCTGTGGCCTCACCCACAGGGC                              1292
```

FIGURE 18A

1	M	E	L	S	P	N	A	S	T	G	L	L	S	C	N	D	S	E	F	K	20
21	E	H	F	D	L	E	D	L	N	L	T	H	E	D	L	R	L	K	Y	L	40
41	G	P	Q	Q	V	K	Q	F	L	P	I	C	V	T	Y	L	L	I	F	V	60
61	V	G	T	L	G	N	G	L	T	C	T	V	I	L	R	Q	K	A	M	H	80
81	T	P	T	N	F	Y	L	F	S	L	A	V	S	D	L	L	V	L	L	V	100
101	G	L	P	L	E	L	Y	E	M	Q	H	N	Y	P	F	Q	L	G	A	G	120
121	G	C	Y	F	R	I	L	L	L	E	T	V	C	L	A	S	V	L	N	V	140
141	T	A	L	S	V	E	R	Y	V	A	V	V	H	P	L	Q	A	K	S	V	160
161	M	T	R	T	H	V	R	R	M	L	G	A	I	W	V	F	A	I	L	F	180
181	S	L	P	N	T	S	L	H	G	L	S	P	L	Y	V	P	C	R	G	P	200
201	V	P	D	S	V	T	C	T	L	V	R	P	Q	F	F	Y	K	L	V	I	220
221	Q	T	T	I	L	L	F	F	C	L	P	M	V	T	I	S	V	L	Y	L	240

FIGURE 18B

241	L I G L R L R R E R M L L Q E E V K G R	260
261	I S A A A R Q A S H R S I Q L R D R E R	280
281	R Q V T K M L I A L V I V F G T C W V P	300
301	F H A D R L M W S M V S H W T D G L R L	320
321	A F Q S V H L A S G V F L Y L G S A A N	340
341	P E L Y N L M S T R F R E S F R E T L G	360
361	L G T R C C H R H Q P R H D S H S H L R	380
381	L T T V S T L C D R N S R D V P L A E N	400
401	R D P G C E Q E T D P P E	413

FIGURE 19A

```
   1  GGGACAGCACGTTAGACCCAAGTCTCATGGACTTCCTCTCTCAGTGTCATTTTTTTCTCA   60
  61  TCTGTAAAATGGGATTGTTGTCCAGAAAAAGGAGACATTCTCAGCTTCGGCTCTCCCCAA  120
 121  ATGCTTCAACGGGCCTCTTGTCCTGCAATGACAGTGAGTTCAAGGAGCACTTTGACCTTG  180
 181  AGGACCTGAACCTTACTCATGAGGACCTGAGGCTGAAGTACTTGGGGCCACAGCAGGTAA  240
 241  AACAATTTTTGCCCATCTGTGTCACGTACCTGTTGATCTTCGTAGTGGGCACTCTGGGCA  300
 301  ACGGGTTGACCTGCACCGTCATCCTGCGCCAGAAGGCAATGCACACGCCCACCAACTTCT  360
 361  ACCTCTTCAGTCTCGCGGTGTCCGATTTGCTGGTGCTCCTGGTGGGCTTGCCCCTGGAAC  420
 421  TTTATGAGATGCAGCACAATTACCCATTCCAGCTGGGTGCAGGTGGCTGTTACTTCCGGA  480
 481  TACTGCTTTTGGAGACTGTCTGCCTGGCTTCAGTGCTCAATGTCACAGCCCTAAGTGTGG  540
 541  AGCGTTATGTGGCCGTGGTGCACCCACTCCAAGCCAAGTCTGTGATGACACGGACCCATG  600
 601  TGCGCCGCATGTTGGGAGCCATCTGGGTCTTCGCTATTCTCTTCTCTCTGCCCAACACCA  660
 661  GCTTACATGGCCTCAGTCCACTCTATGTACCCTGCCGGGGGCCGGTGCCCGATTCAGTTA  720
```

FIGURE 19B

```
721  CGTGTACGCTGGTGCGTCCCCAGTTCTTCTACAAGTTGGTAATACAGACGACCATACTGC  780
781  TCTTCTTCTGTCTGCCCATGGTCACCATCAGTGTGCTGTACCTGCTCATTGGGCTGAGGC  840
841  TGCGGAGGGAGAGGATGTTGCTCCAAGAGGAGGTCAAGGGCAGGATATCTGCAGCAGCCA  900
901  GGCAGGCCTCCCACAGAAGTATTCAGCTTCGAGATAGGGAACGCAGACAGGTGACCAAGA  960
961  TGCTAATTGCTCTGGTTATAGTATTTGGCACCTGCTGGGTTCCATTCCATGCTGACCGTC 1020
1021 TCATGTGGAGTATGGTGTCCCATTGGACTGACGGCCTGCGCCTGGCCTTCCAGTCTGTGC 1080
1081 ACCTTGCTTCTGGTGTCTTCTTGTACCTCGGCTCAGCGGCTAACCCGGAGCTCTACAACC 1140
1141 TCATGTCCACTCGCTTCCGAGAGTCCTTCCGGGAAACCCTGGGCCTTGGGACACGGTGCT 1200
1201 GTCATCGCCACCAACCGCGTCACGACTCCCATAGCCACCTTAGGTTGACCACAGTCAGCA 1260
1261 CCCTGTGTGACAGGAACAGCAGGGATGTACCCCTGGCTGAGAACAGGGATCCAGGGTGTG 1320
1321 AGCAAGAGACAGACCCTCCTGAATAAAATCCTGTGGCCTCACCCACAGGGC          1371
```

FIGURE 20A

1	M	D	F	L	S	Q	C	H	F	F	L	I	C	K	M	G	L	L	S	R	20
21	K	R	R	H	S	Q	L	R	L	S	P	N	A	S	T	G	L	L	S	C	40
41	N	D	S	E	F	K	E	H	F	D	L	E	D	L	N	L	T	H	E	D	60
61	L	R	L	K	Y	L	G	P	Q	Q	V	K	Q	F	L	P	I	C	V	T	80
81	Y	L	L	I	F	V	V	G	T	L	G	N	G	L	T	C	T	V	I	L	100
101	R	Q	K	A	M	H	T	P	T	N	F	Y	L	F	S	L	A	V	S	D	120
121	L	L	V	L	L	V	G	L	P	L	E	L	Y	E	M	Q	H	N	Y	P	140
141	F	Q	L	G	A	G	G	C	Y	F	R	I	L	L	L	E	T	V	C	L	160
161	A	S	V	L	N	V	T	A	L	S	V	E	R	Y	V	A	V	V	H	P	180
181	L	Q	A	K	S	V	M	T	R	T	H	V	R	R	M	L	G	A	I	W	200
201	V	F	A	I	L	F	S	L	P	N	T	S	L	H	G	L	S	P	L	Y	220
221	V	P	C	R	G	P	V	P	D	S	V	T	C	T	L	V	R	P	Q	F	240

FIGURE 20B

241	F	Y	K	L	V	I	Q	T	T	I	L	L	F	F	C	L	P	M	V	T	260
261	I	S	V	L	Y	L	L	I	G	L	R	L	R	R	E	R	M	L	L	Q	280
281	E	E	V	K	G	R	I	S	A	A	A	R	Q	A	S	H	R	S	I	Q	300
301	L	R	D	R	E	R	R	Q	V	T	K	M	L	I	A	L	V	I	V	F	320
321	G	T	C	W	V	P	F	H	A	D	R	L	M	W	S	M	V	S	H	W	340
341	T	D	G	L	R	L	A	F	Q	S	V	H	L	A	S	G	V	F	L	Y	360
361	L	G	S	A	A	N	P	E	L	Y	N	L	M	S	T	R	F	R	E	S	380
381	F	R	E	T	L	G	L	G	T	R	C	C	H	R	H	Q	P	R	H	D	400
401	S	H	S	H	L	R	L	T	T	V	S	T	L	C	D	R	N	S	R	D	420
421	V	P	L	A	E	N	R	D	P	G	C	E	Q	E	T	D	P	P	E		439

FIGURE 21A

```
Rat SNORF62a  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~MELS PNASTGLLSC NDSEFKEHFD
Rat SNORF62b  MDFLSQCHFF LICKMGLLSR KRRHSQLRLS PNASTGLLSC NDSEFKEHFD
Hum SNORF62   ~~~~~~~~~~ ~~~~MTPLCL NCSVLPGDLY PGGARNPMAC NGSAARGHFD

Rat SNORF62a  LEDLNLTHED LRLKYLGPQQ VKQFLPICVT YLLIFVVGTL GNGLTCTVIL
Rat SNORF62b  LEDLNLTHED LRLKYLGPQQ VKQFLPICVT YLLIFVVGTL GNGLTCTVIL
Hum SNORF62   PEDLNLTDEA LRLKYLGPQQ TELFMPICAT YLLIFVVGAV GNGLTCLVIL

Rat SNORF62a  RQKAMHTPTN FYLFSLAVSD LLVLLVGLPL ELYEMQHNYP FQLGAGGCYF
Rat SNORF62b  RQKAMHTPTN FYLFSLAVSD LLVLLVGLPL ELYEMQHNYP FQLGAGGCYF
Hum SNORF62   RHKAMRTPTN YYLFSLAVSD LLVLLVGLPL ELYEMWHNYP FLLGVGGCYF

Rat SNORF62a  RILLLETVCL ASVLNVTALS VERYVAVVHP LQAKSVMTRT HVRRMLGAIW
Rat SNORF62b  RILLLETVCL ASVLNVTALS VERYVAVVHP LQAKSVMTRT HVRRMLGAIW
Hum SNORF62   RTLLFEMVCL ASVLNVTALS VERYVAVVHP LQARSMVTRA HVRRVLGAVW
```

FIGURE 21B

```
Rat SNORF62a  VFAILFSLPN TSLHGLSPLY VPCRGPVPDS VTCTLVRPQF FYKLVIQTTI
Rat SNORF62b  VFAILFSLPN TSLHGLSPLY VPCRGPVPDS VTCTLVRPQF FYKLVIQTTI
Hum SNORF62   GLAMLCSLPN TSLHGIRQLH VPCRGPVPDS AVCMLVRPRA LYNMVVQTTA

Rat SNORF62a  LLFFCLPMVT ISVLYLLIGL RLRRERMLLQ EEVKGRISAA ARQASHRSIQ
Rat SNORF62b  LLFFCLPMVT ISVLYLLIGL RLRRERMLLQ EEVKGRISAA ARQASHRSIQ
Hum SNORF62   LLFFCLPMAI MSVLYLLIGL RLRRERLLLM QEAKGRGSAA ARSRYTCRLQ

Rat SNORF62a  LRDRERRQVT KMLIALVIVF GTCWVPFHAD RLMWSMVSHW TDGLRLAFQS
Rat SNORF62b  LRDRERRQVT KMLIALVIVF GTCWVPFHAD RLMWSMVSHW TDGLRLAFQS
Hum SNORF62   QHDRGRRQVT KMLFVLVVVF GICWAPFHAD RVMWSVVSQW TDGLHLAFQH

Rat SNORF62a  VHLASGVFLY LGSAANPELY NLMSTRFRES FRETLGLGTR CCHRHQPRHD
Rat SNORF62b  VHLASGVFLY LGSAANPELY NLMSTRFRES FRETLGLGTR CCHRHQPRHD
Hum SNORF62   VHVISGIFFY LGSAANPVLY SLMSSRFRET FQEALCLGA. CCHRLRPRHS
```

FIGURE 21C

```
Rat SNORF62a   SHSHLRLTTV STLCDRNSRD V...PLAENR DPGCEQETDP PE
Rat SNORF62b   SHSHLRLTTV STLCDRNSRD V...PLAENR DPGCEQETDP PE
Hum SNORF62    SHSLSRMTTG STLCDVGSLG SWVHPLAGND GPEAQQETDP S~~
```

FIGURE 22

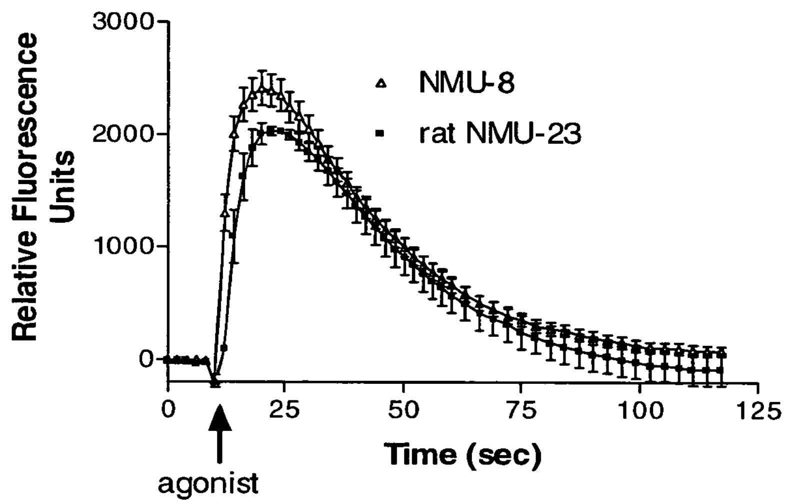

FIGURE 23